

Polynucleotide SEQ ID NO: 1; Polypeptide SEQ ID NO: 2



aattccgttg	ctgtcgggttc	agtccaagtc	tcctccagtg	caaaatgaga	aatgggtggtc	60
gccattacag	gaacatgcac	tacatctgtg	ttaatgaaat	attgtcagtt	atctgaaggt	120
tattaaaatg	tttctgcaag	gatggcttca	cgagaaatca	attctgcacg	ttttccatt	180
gtcattgtat	gaataactga	ccaaagggat	gtaacaaaat	ggaacaaagc	tgaggaccac	240
gttcaccctt	tcttgaggca	tacgatcaac	cctgaaggag	atggaagact	tgaggaggaa	300
atggggattg	atcttccagg	agttctgctg	taaagcgatc	cctcaccatt	acaaagataa	360
gcagaaatcc	tccaggcatc	ctctgtaaac	gggctggcgt	agtgtggctt	ggtcaaggaa	420
cagagacagg	gctgcaca	atg gct cag ctt cac tgc	caa ctc tta ttc ttg			471
		Met Ala Gln Leu His Cys	Gln Leu Leu Phe Leu			
	1		5		10	
gga ttt aca ctc cta cag tcg tac aat gtc tca ggg tat ggt cca aac						519
Gly Phe Thr Leu Leu Gln Ser Tyr Asn Val Ser Gly Tyr Gly Pro Asn						
	15		20		25	
caa agg gcc cag aag aaa gga gac atc ata ctg gga ggt ctc ttc cca						567
Gln Arg Ala Gln Lys Lys Gly Asp Ile Ile Leu Gly Gly Leu Phe Pro						
	30		35		40	
ata cac ttt gga gta gcc gcc aag gat cag gac tta aaa tcg aga ccg						615
Ile His Phe Gly Val Ala Ala Lys Asp Gln Asp Leu Lys Ser Arg Pro						
	45		50		55	
gag gcg aca aaa tgt att cgg tac aat ttt cga ggc ttc cga tgg ctc						663
Glu Ala Thr Lys Cys Ile Arg Tyr Asn Phe Arg Gly Phe Arg Trp Leu						
	60		65		70	75
cag gcg atg ata ttc gca att gaa gag att aac aac agt atg act ttc						711
Gln Ala Met Ile Phe Ala Ile Glu Glu Ile Asn Asn Ser Met Thr Phe						
	80		85		90	
ctg ccc aat atc acc ctg gga tat cgc ata ttt gac acg tgt aac acc						759
Leu Pro Asn Ile Thr Leu Gly Tyr Arg Ile Phe Asp Thr Cys Asn Thr						
	95		100		105	
gtg tcc aag gcg cta gag gca aca ctc agc ttt gtg gcc cag aac aaa						807
Val Ser Lys Ala Leu Glu Ala Thr Leu Ser Phe Val Ala Gln Asn Lys						
	110		115		120	
atc gac tcg ctg aac tta gat gag ttc tgt aac tgc tct gac cat atc						855
Ile Asp Ser Leu Asn Leu Asp Glu Phe Cys Asn Cys Ser Asp His Ile						
	125		130		135	
cca tcc aca ata gca gtg gtc ggg gca acc ggg tca gga atc tcc acg						903
Pro Ser Thr Ile Ala Val Val Gly Ala Thr Gly Ser Gly Ile Ser Thr						
	140		145		150	155
gct gtg gcc aat cta ttg gga tta ttt tac att cca cag gtc agc tat						951
Ala Val Ala Asn Leu Leu Gly Leu Phe Tyr Ile Pro Gln Val Ser Tyr						
	160		165		170	
gcc tcc tcg agc agg ctg ctc agc aac aag aat gag tac aag gcc ttc						999
Ala Ser Ser Ser Arg Leu Leu Ser Asn Lys Asn Glu Tyr Lys Ala Phe						
	175		180		185	
ctg agg acc atc ccc aat gat gag caa cag gcc acg gcc atg gcc gag						1047
Leu Arg Thr Ile Pro Asn Asp Glu Gln Gln Ala Thr Ala Met Ala Glu						
	190		195		200	

FIG. 4A

Polynucleotide SEQ ID NO: 1; Polypeptide SEQ ID NO: 2 (CONTINUED)

atc	atc	gag	cac	ttc	cag	tgg	aac	tgg	gtg	gga	acc	ctg	gca	gcc	gac	1095
Ile	Ile	Glu	His	Phe	Gln	Trp	Asn	Trp	Val	Gly	Thr	Leu	Ala	Ala	Asp	
205						210					215					
gat	gac	tat	ggc	cgc	cca	ggc	att	gac	aag	ttc	cgg	gag	gag	gcc	gtt	1143
Asp	Asp	Tyr	Gly	Arg	Pro	Gly	Ile	Asp	Lys	Phe	Arg	Glu	Glu	Ala	Val	
220					225					230					235	
aag	agg	gac	atc	tgt	att	gac	ttc	agt	gag	atg	atc	tct	cag	tac	tac	1191
Lys	Arg	Asp	Ile	Cys	Ile	Asp	Phe	Ser	Glu	Met	Ile	Ser	Gln	Tyr	Tyr	
				240					245					250		
acc	cag	aag	cag	ttg	gag	ttc	atc	gcc	gac	gtc	atc	cag	aac	tcc	tcc	1239
Thr	Gln	Lys	Gln	Leu	Glu	Phe	Ile	Ala	Asp	Val	Ile	Gln	Asn	Ser	Ser	
			255					260					265			
gcc	aag	gtc	atc	gtg	gtc	ttc	tcc	aat	ggc	ccc	gac	ctg	gag	ccg	ctc	1287
Ala	Lys	Val	Ile	Val	Val	Phe	Ser	Asn	Gly	Pro	Asp	Leu	Glu	Pro	Leu	
		270					275					280				
atc	cag	gag	ata	gtt	cgg	aga	aac	atc	acc	gat	cgg	atc	tgg	ctg	gcc	1335
Ile	Gln	Glu	Ile	Val	Arg	Arg	Asn	Ile	Thr	Asp	Arg	Ile	Trp	Leu	Ala	
	285					290					295					
agc	gag	gct	tgg	gcc	agc	tct	tcc	ctc	att	gcc	aag	cca	gag	tac	ttc	1383
Ser	Glu	Ala	Trp	Ala	Ser	Ser	Ser	Leu	Ile	Ala	Lys	Pro	Glu	Tyr	Phe	
300					305					310					315	
cac	gtg	gtc	ggc	ggc	acc	atc	ggc	ttc	gct	ctc	agg	gcg	ggg	cgt	atc	1431
His	Val	Val	Gly	Gly	Thr	Ile	Gly	Phe	Ala	Leu	Arg	Ala	Gly	Arg	Ile	
				320				325						330		
cca	ggg	ttc	aac	aag	ttc	ctg	aag	gag	gtc	cac	ccc	agc	agg	tcc	tcc	1479
Pro	Gly	Phe	Asn	Lys	Phe	Leu	Lys	Glu	Val	His	Pro	Ser	Arg	Ser	Ser	
			335					340				345				
gac	aat	ggg	ttt	gtc	aag	gag	ttc	tgg	gag	gag	acc	ttc	aac	tgc	tac	1527
Asp	Asn	Gly	Phe	Val	Lys	Glu	Phe	Trp	Glu	Glu	Thr	Phe	Asn	Cys	Tyr	
		350					355					360				
ttc	acc	gag	aag	acc	ctg	acg	cag	ctg	aag	aat	tcc	aag	gtg	ccc	tcc	1575
Phe	Thr	Glu	Lys	Thr	Leu	Thr	Gln	Leu	Lys	Asn	Ser	Lys	Val	Pro	Ser	
	365					370					375					
cac	gga	ccg	gcg	gct	caa	ggg	gac	ggc	tcc	aag	gcg	ggg	aac	tcc	aga	1623
His	Gly	Pro	Ala	Ala	Gln	Gly	Asp	Gly	Ser	Lys	Ala	Gly	Asn	Ser	Arg	
380					385				390						395	
cgg	aca	gcc	cta	cgc	cac	ccc	tgc	act	ggg	gag	gag	aac	atc	acc	agc	1671
Arg	Thr	Ala	Leu	Arg	His	Pro	Cys	Thr	Gly	Glu	Glu	Asn	Ile	Thr	Ser	
				400				405					410			
gtg	gag	acc	ccc	tac	ctg	gat	tat	aca	cac	ctg	agg	atc	tcc	tac	aat	1719
Val	Glu	Thr	Pro	Tyr	Leu	Asp	Tyr	Thr	His	Leu	Arg	Ile	Ser	Tyr	Asn	
			415					420					425			
gta	tac	gtg	gcc	gtc	tac	tcc	att	gct	cac	gcc	ctg	caa	gac	atc	cac	1767
Val	Tyr	Val	Ala	Val	Tyr	Ser	Ile	Ala	His	Ala	Leu	Gln	Asp	Ile	His	
		430					435					440				

FIG. 4B

Polynucleotide SEQ ID NO: 1; Polypeptide SEQ ID NO: 2 (CONTINUED)

tct tgc aaa ccc ggc acg-ggc atc ttt gca aac gga tct tgt gca gat	1815
Ser Cys Lys Pro Gly Thr Gly Ile Phe Ala Asn Gly Ser Cys Ala Asp	
445 450 455	
att aaa aaa gtt gag gcc tgg cag gtc ctc aac cat ctg ctg cat ctg	1863
Ile Lys Lys Val Glu Ala Trp Gln Val Leu Asn His Leu Leu His Leu	
460 465 470 475	
aag ttt acc aac agc atg ggt gag cag gtt gac ttt gac gat caa ggt	1911
Lys Phe Thr Asn Ser Met Gly Glu Gln Val Asp Phe Asp Asp Gln Gly	
480 485 490	
gac ctc aag ggg aac tac acc att atc aac tgg cag ctc tcc gca gag	1959
Asp Leu Lys Gly Asn Tyr Thr Ile Ile Asn Trp Gln Leu Ser Ala Glu	
495 500 505	
gat gaa tcg gtg ttg ttc cat gag gtg ggc aac tac aac gcc tac gct	2007
Asp Glu Ser Val Leu Phe His Glu Val Gly Asn Tyr Asn Ala Tyr Ala	
510 515 520	
aag ccc agt gac cga ctc aac atc aac gaa aag aaa atc ctc tgg agt	2055
Lys Pro Ser Asp Arg Leu Asn Ile Asn Glu Lys Lys Ile Leu Trp Ser	
525 530 535	
ggc ttc tcc aaa gtg gtt cct ttc tcc aac tgc agt cga gac tgt gtg	2103
Gly Phe Ser Lys Val Val Pro Phe Ser Asn Cys Ser Arg Asp Cys Val	
540 545 550 555	
ccg ggc acc agg aag ggg atc atc gag ggg gag ccc acc tgc tgc ttt	2151
Pro Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr Cys Cys Phe	
560 565 570	
gaa tgc atg gca tgt gca gag gga gag ttc agt gat gaa aac gat gca	2199
Glu Cys Met Ala Cys Ala Glu Gly Glu Phe Ser Asp Glu Asn Asp Ala	
575 580 585	
agt gcg tgt aca aag tgc ccg aat gat ttc tgg tcg aat gag aac cac	2247
Ser Ala Cys Thr Lys Cys Pro Asn Asp Phe Trp Ser Asn Glu Asn His	
590 595 600	
acg tcg tgc atc gcc aag gag atc gag tac ctg tcg tgg acg gag ccc	2295
Thr Ser Cys Ile Ala Lys Glu Ile Glu Tyr Leu Ser Trp Thr Glu Pro	
605 610 615	
ttc ggg atc gct ctg acc atc ttc gcc gta ctg ggc atc ctg atc acc	2343
Phe Gly Ile Ala Leu Thr Ile Phe Ala Val Leu Gly Ile Leu Ile Thr	
620 625 630 635	
tcc ttc gtg ctg ggg gtc ttc atc aag ttc agg aac act ccc atc gtg	2391
Ser Phe Val Leu Gly Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val	
640 645 650	
aag gcc acc aac cgg gag ttg tcc tac ctg ctg ctc ttc tcc ctc atc	2439
Lys Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe Ser Leu Ile	
655 660 665	
tgc tgc ttc tcc agc tcg ctc atc ttc atc ggc gag ccc agg gac tgg	2487
Cys Cys Phe Ser Ser Ser Leu Ile Phe Ile Gly Glu Pro Arg Asp Trp	
670 675 680	

Polynucleotide SEQ ID NO: 1; Polypeptide SEQ ID NO: 2 (CONTINUED)

acc	tgt	cgg	ctc	cgc	caa	-ccg	gcc	ttt	ggc	atc	agc	ttc	gtc	ctg	tgc	2535
Thr	Cys	Arg	Leu	Arg	Gln	Pro	Ala	Phe	Gly	Ile	Ser	Phe	Val	Leu	Cys	
	685					690					695					
atc	tcc	tgc	atc	ctg	gtg	aag	acc	aac	cgg	gtg	ctg	ctg	gtc	ttc	gag	2583
Ile	Ser	Cys	Ile	Leu	Val	Lys	Thr	Asn	Arg	Val	Leu	Leu	Val	Phe	Glu	
700					705					710					715	
gcc	aag	atc	ccc	acc	agc	ctc	cac	cgc	aag	tgg	gtg	ggc	ctc	aac	ctg	2631
Ala	Lys	Ile	Pro	Thr	Ser	Leu	His	Arg	Lys	Trp	Val	Gly	Leu	Asn	Leu	
				720					725					730		
cag	ttc	ctc	ctg	gtc	ttc	ctc	tgc	atc	ctg	gtg	caa	atc	gtc	acc	tgc	2679
Gln	Phe	Leu	Leu	Val	Phe	Leu	Cys	Ile	Leu	Val	Gln	Ile	Val	Thr	Cys	
			735					740					745			
atc	atc	tgg	ctc	tac	acc	gcg	cct	ccc	tcc	agc	tac	agg	aac	cat	gag	2727
Ile	Ile	Trp	Leu	Tyr	Thr	Ala	Pro	Pro	Ser	Ser	Tyr	Arg	Asn	His	Glu	
		750					755					760				
ctg	gag	gac	gag	gtc	atc	ttc	atc	acc	tgc	gac	gag	ggc	tgc	ctc	atg	2775
Leu	Glu	Asp	Glu	Val	Ile	Phe	Ile	Thr	Cys	Asp	Glu	Gly	Ser	Leu	Met	
	765					770					775					
gcg	ctg	ggc	ttc	ctc	atc	ggc	tac	acc	tgc	ctc	ctc	gcc	gcc	atc	tgc	2823
Ala	Leu	Gly	Phe	Leu	Ile	Gly	Tyr	Thr	Cys	Leu	Leu	Ala	Ala	Ile	Cys	
780					785				790						795	
ttc	ttc	ttc	gcc	ttc	aag	tcc	cgt	aag	ctg	ccg	gag	aac	ttc	aac	gag	2871
Phe	Phe	Phe	Ala	Phe	Lys	Ser	Arg	Lys	Leu	Pro	Glu	Asn	Phe	Asn	Glu	
			800						805				810			
gct	aag	ttc	atc	acc	ttc	agc	atg	ttg	atc	ttc	ttc	atc	gtc	tgg	atc	2919
Ala	Lys	Phe	Ile	Thr	Phe	Ser	Met	Leu	Ile	Phe	Phe	Ile	Val	Trp	Ile	
			815					820					825			
tcc	ttc	atc	ccc	gcc	tat	gtc	agc	acc	tac	ggc	aag	ttt	gtg	tgc	gcc	2967
Ser	Phe	Ile	Pro	Ala	Tyr	Val	Ser	Thr	Tyr	Gly	Lys	Phe	Val	Ser	Ala	
		830					835					840				
gtg	gag	gtg	att	gcc	atc	ctg	gcc	tcc	agc	ttc	ggg	ctg	ctg	ggc	tgc	3015
Val	Glu	Val	Ile	Ala	Ile	Leu	Ala	Ser	Ser	Phe	Gly	Leu	Leu	Gly	Cys	
	845					850					855					
att	tac	ttc	aac	aag	tgt	tac	atc	atc	ctg	ttc	aag	ccg	tgc	cgt	aac	3063
Ile	Tyr	Phe	Asn	Lys	Cys	Tyr	Ile	Ile	Leu	Phe	Lys	Pro	Cys	Arg	Asn	
860					865					870					875	
acc	atc	gag	gag	gtg	cgc	tgc	agc	acg	gcg	gcc	cac	gcc	ttc	aag	gtg	3111
Thr	Ile	Glu	Glu	Val	Arg	Cys	Ser	Thr	Ala	Ala	His	Ala	Phe	Lys	Val	
				880					885					890		
gcg	gcc	cgg	gcc	acc	ctc	cgg	cgc	agc	gcc	gcg	tct	cgc	aag	cgc	tcc	3159
Ala	Ala	Arg	Ala	Thr	Leu	Arg	Arg	Ser	Ala	Ala	Ser	Arg	Lys	Arg	Ser	
			895					900					905			
agc	agc	ctg	tgc	ggc	tcc	acc	atc	tcc	tgc	ccc	gcc	tgc	tcc	acc	tgc	3207
Ser	Ser	Leu	Cys	Gly	Ser	Thr	Ile	Ser	Ser	Pro	Ala	Ser	Ser	Thr	Cys	
		910					915					920				

Polynucleotide SEQ ID NO: 1; Polypeptide SEQ ID NO: 2 (CONTINUED)

ggg ccg ggc ctc acc atg gag atg cag cgc tgc agc acg cag aag gtc	3255
Gly Pro Gly Leu Thr Met Glu Met Gln Arg Cys Ser Thr Gln Lys Val	
925 930 935	
agc ttc ggc agc ggc acc gtc acc ctg tcg ctc agc ttc gag gag aca	3303
Ser Phe Gly Ser Gly Thr Val Thr Leu Ser Leu Ser Phe Glu Glu Thr	
940 945 950 955	
ggc cga tac gcc acc ctc agc cgc acg gcc cgc agc agg aac tcg gcg	3351
Gly Arg Tyr Ala Thr Leu Ser Arg Thr Ala Arg Ser Arg Asn Ser Ala	
960 965 970	
gat ggc cgc agc ggc gac gac ctg cca tct aga cac cac gac cag ggc	3399
Asp Gly Arg Ser Gly Asp Asp Leu Pro Ser Arg His His Asp Gln Gly	
975 980 985	
ccg cct cag aaa tgc gag ccc cag ccc gcc aac gat gcc cga tac aag	3447
Pro Pro Gln Lys Cys Glu Pro Gln Pro Ala Asn Asp Ala Arg Tyr Lys	
990 995 1000	
gcg gcg ccg acc aag ggc acc cta gag tcg ccg ggc ggc agc aag gag	3495
Ala Ala Pro Thr Lys Gly Thr Leu Glu Ser Pro Gly Gly Ser Lys Glu	
1005 1010 1015	
cgc ccc aca act atg gag gaa acc taa tccaactcct ccatcaaccc	3542
Arg Pro Thr Thr Met Glu Glu Thr *	
1020 1025	
caagaacatc ctccaacggca gcaccgtcga caactgacat caactcctaa ccggtggctg	3602
cccaacctct cccctctccg gcacttttgcg ttttgctgaa gattgcagca tctgcagttc	3662
cttttatccc tgattttctg acttgatat ttactagtgt gcgatggaat atcacaacat	3722
aatgagttgc acaattaggt gagcagagtt gtgtcaaagt atctgaacta tctgaagtat	3782
ctgaactact ttattctctc gaattgtatt acaaacattt gaagtatttt tagtgacatt	3842
atgttctaac attgtcaaga taatttggtta caacatatataa ggtaccacct gaagcagtga	3902
ctgagattgc cactgtgatg acagaactgt tttataacat ttatcattga aacctggatt	3962
gcaacaggaa tataatgact gtaacaaaaa aattgttgat tatcttaaaa atgcaaattg	4022
taatcagatg tgtaaaattg gtaattactt ctgtacatta aatgcatatt tcttgataaa	4082
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaagcggcc cgacagcaac gg	4134

FIG. 4E

Polynucleotide SEQ ID NO: 1; Polypeptide SEQ ID NO: 2

aattccggtg	ctgtcgggtc	agtccaagtc	tcctccagtg	caaaatgaga	aatgggtggtc	60
gccattacag	gaacatgcac	tacatctgtg	ttaatgaaat	attgtcagtt	atctgaaggt	120
tattaaaatg	tttctgcaag	gatggcttca	cgagaaatca	attctgcacg	ttttcccatt	180
gtcattgtat	gaataactga	ccaaagggat	gtaacaaaat	ggaacaaagc	tgaggaccac	240
gttcaccctt	tcttgagca	tacgatcaac	cctgaaggag	atggaagact	tgaggaggaa	300
atggggattg	atcttccagg	agttctgctg	taaagcgatc	cctcaccatt	acaaagataa	360
gcagaaatcc	tccaggcatc	ctctgtaaac	gggctggcgt	agtgtggctt	ggccaaggaa	420
cagagacagg	gctgcaca	atg gct cag	ctt cac tgc	caa ctc tta	ttc ttg	471
	Met	Ala	Gln	Leu	His	Cys
	1			5		
						10
gga ttt aca ctc cta cag tgc tac aat gtc tca ggg tat ggt cca aac						519
Gly Phe Thr Leu Leu Gln Ser Tyr Asn Val Ser Gly Tyr Gly Pro Asn						
	15			20		25
caa agg gcc cag aag aaa gga gac atc ata ctg gga ggt ctc ttc cca						567
Gln Arg Ala Gln Lys Lys Gly Asp Ile Ile Leu Gly Gly Leu Phe Pro						
	30			35		40
ata cac ttt gga gta gcc gcc aag gat cag gac tta aaa tgc aga ccg						615
Ile His Phe Gly Val Ala Ala Lys Asp Gln Asp Leu Lys Ser Arg Pro						
	45			50		55
gag gcg aca aaa tgt att cgg tac aat ttt cga ggc ttc cga tgg ctc						663
Glu Ala Thr Lys Cys Ile Arg Tyr Asn Phe Arg Gly Phe Arg Trp Leu						
	60			65		70
cag gcg atg ata ttc gca att gaa gag att aac aac agt atg act ttc						711
Gln Ala Met Ile Phe Ala Ile Glu Glu Ile Asn Asn Ser Met Thr Phe						
		80			85	90
ctg ccc aat atc acc ctg gga tat cgc ata ttt gac acg tgt aac acc						759
Leu Pro Asn Ile Thr Leu Gly Tyr Arg Ile Phe Asp Thr Cys Asn Thr						
		95			100	105
gtg tcc aag gcg cta gag gca aca ctc agc ttt gtg gcc cag aac aaa						807
Val Ser Lys Ala Leu Glu Ala Thr Leu Ser Phe Val Ala Gln Asn Lys						
	110			115		120
atc gac tgc ctg aac tta gat gag ttc tgt aac tgc tct gac cat atc						855
Ile Asp Ser Leu Asn Leu Asp Glu Phe Cys Asn Cys Ser Asp His Ile						
	125			130		135
cca tcc aca ata gca gtg gtc ggg gca acc ggg tca gga atc tcc acg						903
Pro Ser Thr Ile Ala Val Val Gly Ala Thr Gly Ser Gly Ile Ser Thr						
	140			145		150
gct gtg gcc aat cta ttg gga tta ttt tac att cca cag gtc agc tat						951
Ala Val Ala Asn Leu Leu Gly Leu Phe Tyr Ile Pro Gln Val Ser Tyr						
		160			165	170
gcc tcc tgc agc agg ctg ctc agc aac aag aat gag tac aag gcc ttc						999
Ala Ser Ser Ser Arg Leu Leu Ser Asn Lys Asn Glu Tyr Lys Ala Phe						
		175			180	185
ctg agg acc atc ccc aat gat gag caa cag gcc acg gcc atg gcc gag						1047
Leu Arg Thr Ile Pro Asn Asp Glu Gln Gln Ala Thr Ala Met Ala Glu						
	190				195	200

Polynucleotide SEQ ID NO: 1; Polypeptide SEQ ID NO: 2 (CONTINUED)

atc atc gag cac ttc dag tgg aac tgg gtg gga acc ctg gca gcc gac Ile Ile Glu His Phe Gln Trp Asn Trp Val Gly Thr Leu Ala Ala Asp 205 210 215	1095
gat gac tat ggc cgc cca ggc att gac aag ttc cgg gag gag gcc gtt Asp Asp Tyr Gly Arg Pro Gly Ile Asp Lys Phe Arg Glu Glu Ala Val 220 225 230 235	1143
aag agg gac atc tgt att gac ttc agt gag atg atc tct cag tac tac Lys Arg Asp Ile Cys Ile Asp Phe Ser Glu Met Ile Ser Gln Tyr Tyr 240 245 250	1191
acc cag aag cag ttg gag ttc atc gcc gac gtc atc cag aac tcc tcg Thr Gln Lys Gln Leu Glu Phe Ile Ala Asp Val Ile Gln Asn Ser Ser 255 260 265	1239
gcc aag gtc atc gtg gtc ttc tcc aat ggc ccc gac ctg gag ccg ctc Ala Lys Val Ile Val Val Phe Ser Asn Gly Pro Asp Leu Glu Pro Leu 270 275 280	1287
atc cag gag ata gtt cgg aga aac atc acc gat cgg atc tgg ctg gcc Ile Gln Glu Ile Val Arg Arg Asn Ile Thr Asp Arg Ile Trp Leu Ala 285 290 295	1335
agc gag gct tgg gcc agc tct tcg ctc att gcc aag cca gag tac ttc Ser Glu Ala Trp Ala Ser Ser Ser Leu Ile Ala Lys Pro Glu Tyr Phe 300 305 310 315	1383
cac gtg gtc ggc ggc acc atc ggc ttc gct ctc agg gcg ggg cgt atc His Val Val Gly Gly Thr Ile Gly Phe Ala Leu Arg Ala Gly Arg Ile 320 325 330	1431
cca ggg ttc aac aag ttc ctg aag gag gtc cac ccc agc agg tcc tcg Pro Gly Phe Asn Lys Phe Leu Lys Glu Val His Pro Ser Arg Ser Ser 335 340 345	1479
gac aat ggg ttt gtc aag gag ttc tgg gag gag acc ttc aac tgc tac Asp Asn Gly Phe Val Lys Glu Phe Trp Glu Glu Thr Phe Asn Cys Tyr 350 355 360	1527
ttc acc gag aag acc ctg acg cag ctg aag aat tcc aag gtg ccc tcg Phe Thr Glu Lys Thr Leu Thr Gln Leu Lys Asn Ser Lys Val Pro Ser 365 370 375	1575
cac gga ccg gcg gct caa ggg gac ggc tcc aag gcg ggg aac tcc aga His Gly Pro Ala Ala Gln Gly Asp Gly Ser Lys Ala Gly Asn Ser Arg 380 385 390 395	1623
cgg aca gcc cta cgc cac ccc tgc act ggg gag gag aac atc acc agc Arg Thr Ala Leu Arg His Pro Cys Thr Gly Glu Glu Asn Ile Thr Ser 400 405 410	1671
gtg gag acc ccc tac ctg gat tat aca cac ctg agg atc tcc tac aat Val Glu Thr Pro Tyr Leu Asp Tyr Thr His Leu Arg Ile Ser Tyr Asn 415 420 425	1719
gta tac gtg gcc gtc tac tcc att gct cac gcc ctg caa gac atc cac Val Tyr Val Ala Val Tyr Ser Ile Ala His Ala Leu Gln Asp Ile His 430 435 440	1767

Polynucleotide SEQ ID NO: 1; Polypeptide SEQ ID NO: 2 (CONTINUED)

tct tgc aaa ccc ggc acg ggc atc ttt gca aac gga tct tgt gca gat	1815
Ser Cys Lys Pro Gly Thr Gly Ile Phe Ala Asn Gly Ser Cys Ala Asp	
445 450 455	
att aaa aaa gtt gag gcc tgg cag gtc ctc aac cat ctg ctg cat ctg	1863
Ile Lys Lys Val Glu Ala Trp Gln Val Leu Asn His Leu Leu His Leu	
460 465 470 475	
aag ttt acc aac agc atg ggt gag cag gtt gac ttt gac gat caa ggt	1911
Lys Phe Thr Asn Ser Met Gly Glu Gln Val Asp Phe Asp Asp Gln Gly	
480 485 490	
gac ctc aag ggg aac tac acc att atc aac tgg cag ctc tcc gca gag	1959
Asp Leu Lys Gly Asn Tyr Thr Ile Ile Asn Trp Gln Leu Ser Ala Glu	
495 500 505	
gat gaa tcg gtg ttg ttc cat gag gtg ggc aac tac aac gcc tac gct	2007
Asp Glu Ser Val Leu Phe His Glu Val Gly Asn Tyr Asn Ala Tyr Ala	
510 515 520	
aag ccc agt gac cga ctc aac atc aac gaa aag aaa atc ctc tgg agt	2055
Lys Pro Ser Asp Arg Leu Asn Ile Asn Glu Lys Lys Ile Leu Trp Ser	
525 530 535	
ggc ttc tcc aaa gtg gtt cct ttc tcc aac tgc agt cga gac tgt gtg	2103
Gly Phe Ser Lys Val Val Pro Phe Ser Asn Cys Ser Arg Asp Cys Val	
540 545 550 555	
ccg ggc acc agg aag ggg atc atc gag ggg gag ccc acc tgc tgc ttt	2151
Pro Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr Cys Cys Phe	
560 565 570	
gaa tgc atg gca tgt gca gag gga gag ttc agt gat gaa aac gat gca	2199
Glu Cys Met Ala Cys Ala Glu Gly Glu Phe Ser Asp Glu Asn Asp Ala	
575 580 585	
agt gcg tgt aca aag tgc ccg aat gat ttc tgg tcg aat gag aac cac	2247
Ser Ala Cys Thr Lys Cys Pro Asn Asp Phe Trp Ser Asn Glu Asn His	
590 595 600	
acg tcg tgc atc gcc aag gag atc gag tac ctg tcg tgg acg gag ccc	2295
Thr Ser Cys Ile Ala Lys Glu Ile Glu Tyr Leu Ser Trp Thr Glu Pro	
605 610 615	
ttc ggg atc gct ctg acc atc ttc gcc gta ctg ggc atc ctg atc acc	2343
Phe Gly Ile Ala Leu Thr Ile Phe Ala Val Leu Gly Ile Leu Ile Thr	
620 625 630 635	
tcc ttc gtg ctg ggg gtc ttc atc aag ttc agg aac act ccc atc gtg	2391
Ser Phe Val Leu Gly Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val	
640 645 650	
aag gcc acc aac cgg gag ttg tcc tac ctg ctg ctc ttc tcc ctc atc	2439
Lys Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe Ser Leu Ile	
655 660 665	
tgc tgc ttc tcc agc tcg ctc atc ttc atc ggc gag ccc agg gac tgg	2487
Cys Cys Phe Ser Ser Ser Leu Ile Phe Ile Gly Glu Pro Arg Asp Trp	
670 675 680	

Polynucleotide SEQ ID NO: 1; Polypeptide SEQ ID NO: 2 (CONTINUED)

acc	tgt	cgg	ctc	cgc	caa	ccg	gcc	ttt	ggc	atc	agc	ttc	gtc	ctg	tgc	2535
Thr	Cys	Arg	Leu	Arg	Gln	Pro	Ala	Phe	Gly	Ile	Ser	Phe	Val	Leu	Cys	
685						690					695					
atc	tcc	tgc	atc	ctg	gtg	aag	acc	aac	cgg	gtg	ctg	ctg	gtc	ttc	gag	2583
Ile	Ser	Cys	Ile	Leu	Val	Lys	Thr	Asn	Arg	Val	Leu	Leu	Val	Phe	Glu	
700					705					710					715	
gcc	aag	atc	ccc	acc	agc	ctc	cac	cgc	aag	tgg	gtg	ggc	ctc	aac	ctg	2631
Ala	Lys	Ile	Pro	Thr	Ser	Leu	His	Arg	Lys	Trp	Val	Gly	Leu	Asn	Leu	
				720					725					730		
cag	ttc	ctc	ctg	gtc	ttc	ctc	tgc	atc	ctg	gtg	caa	atc	gtc	acc	tgc	2679
Gln	Phe	Leu	Leu	Val	Phe	Leu	Cys	Ile	Leu	Val	Gln	Ile	Val	Thr	Cys	
			735					740					745			
atc	atc	tgg	ctc	tac	acc	gcg	cct	ccc	tcc	agc	tac	agg	aac	cat	gag	2727
Ile	Ile	Trp	Leu	Tyr	Thr	Ala	Pro	Pro	Ser	Ser	Tyr	Arg	Asn	His	Glu	
		750					755					760				
ctg	gag	gac	gag	gtc	atc	ttc	atc	acc	tgc	gac	gag	ggc	tcg	ctc	atg	2775
Leu	Glu	Asp	Glu	Val	Ile	Phe	Ile	Thr	Cys	Asp	Glu	Gly	Ser	Leu	Met	
	765					770					775					
gcg	ctg	ggc	ttc	ctc	atc	ggc	tac	acc	tgc	ctc	ctc	gcc	gcc	atc	tgc	2823
Ala	Leu	Gly	Phe	Leu	Ile	Gly	Tyr	Thr	Cys	Leu	Leu	Ala	Ala	Ile	Cys	
	780				785					790					795	
ttc	ttc	ttc	gcc	ttc	aag	tcc	cgt	aag	ctg	ccg	gag	aac	ttc	aac	gag	2871
Phe	Phe	Phe	Ala	Phe	Lys	Ser	Arg	Lys	Leu	Pro	Glu	Asn	Phe	Asn	Glu	
			800						805				810			
gct	aag	ttc	atc	acc	ttc	agc	atg	ttg	atc	ttc	ttc	atc	gtc	tgg	atc	2919
Ala	Lys	Phe	Ile	Thr	Phe	Ser	Met	Leu	Ile	Phe	Phe	Ile	Val	Trp	Ile	
			815					820					825			
tcc	ttc	atc	ccc	gcc	tat	gtc	agc	acc	tac	ggc	aag	ttt	gtg	tcg	gcc	2967
Ser	Phe	Ile	Pro	Ala	Tyr	Val	Ser	Thr	Tyr	Gly	Lys	Phe	Val	Ser	Ala	
		830					835					840				
gtg	gag	gtg	att	gcc	atc	ctg	gcc	tcc	agc	ttc	ggg	ctg	ctg	ggc	tgc	3015
Val	Glu	Val	Ile	Ala	Ile	Leu	Ala	Ser	Ser	Phe	Gly	Leu	Leu	Gly	Cys	
	845					850					855					
att	tac	ttc	aac	aag	tgt	tac	atc	atc	ctg	ttc	aag	ccg	tgc	cgt	aac	3063
Ile	Tyr	Phe	Asn	Lys	Cys	Tyr	Ile	Ile	Leu	Phe	Lys	Pro	Cys	Arg	Asn	
	860				865					870					875	
acc	atc	gag	gag	gtg	cgc	tgc	agc	acg	gcg	gcc	cac	gcc	ttc	aag	gtg	3111
Thr	Ile	Glu	Glu	Val	Arg	Cys	Ser	Thr	Ala	Ala	His	Ala	Phe	Lys	Val	
				880					885					890		
gcg	gcc	cgg	gcc	acc	ctc	cgg	cgc	agc	gcc	gog	tct	cgc	aag	cgc	tcc	3159
Ala	Ala	Arg	Ala	Thr	Leu	Arg	Arg	Ser	Ala	Ala	Ser	Arg	Lys	Arg	Ser	
			895					900					905			
agc	agc	ctg	tgc	ggc	tcc	acc	atc	tcc	tcg	ccc	gcc	tcg	tcc	acc	tgc	3207
Ser	Ser	Leu	Cys	Gly	Ser	Thr	Ile	Ser	Ser	Pro	Ala	Ser	Ser	Thr	Cys	
		910					915					920				

Docket/App'l'n No.: 10/016,496
Title: POLYCATION-SENSING RECEPTOR ...
Inventors: H. William Harris, *et al.*
Annotated Sheet

cta	cta	gtc	ata	tgg	att	gcg	gcg	gay	gay	gat	tat	ggc	cgc	cca	ggg	48
Leu	Leu	Val	Ile	Trp	Ile	Ala	Ala	Asp	Asp	Asp	Tyr	Gly	Arg	Pro	Gly	
1				5					10					15		
ata	gat	aag	ttt	cga	gaa	gaa	gct	gaa	gag	agg	gac	atc	tgc	ata	gat	96
Ile	Asp	Lys	Phe	Arg	Glu	Glu	Ala	Glu	Glu	Arg	Asp	Ile	Cys	Ile	Asp	
			20					25					30			
ttc	aat	gag	atg	att	tct	cag	tac	tat	aca	caa	aaa	gag	ctg	gag	ttt	144
Phe	Asn	Glu	Met	Ile	Ser	Gln	Tyr	Tyr	Thr	Gln	Lys	Glu	Leu	Glu	Phe	
		35					40					45				
att	gca	gat	act	att	cag	aat	tcc	tca	gcc	aaa	gtg	att	gty	gtc	ttc	192
Ile	Ala	Asp	Thr	Ile	Gln	Asn	Ser	Ser	Ala	Lys	Val	Ile	Xaa	Val	Phe	
	50					55					60					
tca	aat	ggc	cct	gac	ttg	gaa	cca	cta	ata	caa	gag	ata	gtt	cga	cgg	240
Ser	Asn	Gly	Pro	Asp	Leu	Glu	Pro	Leu	Ile	Gln	Glu	Ile	Val	Arg	Arg	
65					70					75					80	
aac	ata	act	gat	aga	ata	tgg	cta	gca	agt	gaa	gcg	tgg	gct	agt	tcc	288
Asn	Ile	Thr	Asp	Arg	Ile	Trp	Leu	Ala	Ser	Glu	Ala	Trp	Ala	Ser	Ser	
				85					90					95		
tca	ctg	ata	gcc	aaa	cca	gaa	tac	ttc	cat	gtt	gtt	ggt	gga	acc	att	336
Ser	Leu	Ile	Ala	Lys	Pro	Glu	Tyr	Phe	His	Val	Val	Gly	Gly	Thr	Ile	
			100					105					110			
gga	ttt	gca	cta	aga	gca	gga	cgc	atc	cca	gga	ttc	cat	gag	ttt	tta	384
Gly	Phe	Ala	Leu	Arg	Ala	Gly	Arg	Ile	Pro	Gly	Phe	His	Glu	Phe	Leu	
		115					120					125				
aaa	aag	gtc	cat	ccc	agc	agg	tcc	tcc	cac	aat	ggc	ttt	gtc	aag	gaa	432
Lys	Lys	Val	His	Pro	Ser	Arg	Ser	Ser	His	Asn	Gly	Phe	Val	Lys	Glu	
	130					135					140					
ttc	tgg	gaa	gaa	aca	ttt	aat	tgt	tat	ttc	act	gaa	gaa	tcc	cta	aca	480
Phe	Trp	Glu	Glu	Thr	Phe	Asn	Cys	Tyr	Phe	Thr	Glu	Glu	Ser	Leu	Thr	
145					150				155						160	
caa	cta	aag	aat	tgc	aaa	aca	cca	acc	cat	gga	tta	gca	atg	cac	aat	528
Gln	Leu	Lys	Asn	Cys	Lys	Thr	Pro	Thr	His	Gly	Leu	Ala	Met	His	Asn	
				165					170					175		
gac	agt	gcg	aaa	atg	ggg	cat	tcc	aca	agg	aca	acg	tta	cga	cct	cca	576
Asp	Ser	Ala	Lys	Met	Gly	His	Ser	Thr	Arg	Thr	Thr	Leu	Arg	Pro	Pro	
			180				185						190			

Polynucleotide SEQ ID NO: 3; Polypeptide SEQ ID NO: 4

tgc	act	gga	gaa	gag	aat	atc	acg	agt	gtg	gag	acc	cct	tac	ctg	gat	624
Cys	Thr	Gly	Glu	Glu	Asn	Ile	Thr	Ser	Val	Glu	Thr	Pro	Tyr	Leu	Asp	
		195					200					205				
tat	act	cac	ctc	cgt	att	tca	tat	aat	gtg	tat	gtg	gca	gtg	tat	tcg	672
Tyr	Thr	His	Leu	Arg	Ile	Ser	Tyr	Asn	Val	Tyr	Val	Ala	Val	Tyr	Ser	
	210					215					220					
att	gct	cac	gct	ctg	cag	gac	atc	tat	gcc	tgc	aca	cct	ggg	aag	ggg	720
Ile	Ala	His	Ala	Leu	Gln	Asp	Ile	Tyr	Ala	Cys	Thr	Pro	Gly	Lys	Gly	
225					230					235					240	
att	ttt	gcg	aac	gga	tca	tgt	gcc	gat	atc	aaa	aaa	gtc	gaa	gcc	tgg	768
Ile	Phe	Ala	Asn	Gly	Ser	Cys	Ala	Asp	Ile	Lys	Lys	Val	Glu	Ala	Trp	
			245						250					255		
aat	cca	tat	gac	tag	t											784
Asn	Pro	Tyr	Asp	*												
			260													

Polynucleotide SEQ ID NO: 3; Polypeptide SEQ ID NO: 4 (CONTINUED)

Leu	Leu	Val	Ile	Trp	Ile	Ala	Ala	Asp	Asp	Asp	Tyr	Gly	Arg	Pro	Gly
1				5					10					15	
Ile	Asp	Lys	Phe	Arg	Glu	Glu	Ala	Glu	Glu	Arg	Asp	Ile	Cys	Ile	Asp
			20					25					30		
Phe	Asn	Glu	Met	Ile	Ser	Gln	Tyr	Tyr	Thr	Gln	Lys	Glu	Leu	Glu	Phe
	35						40					45			
Ile	Ala	Asp	Thr	Ile	Gln	Asn	Ser	Ser	Ala	Lys	Val	Ile	Val	Val	Phe
	50					55					60				
Ser	Asn	Gly	Pro	Asp	Leu	Glu	Pro	Leu	Ile	Gln	Glu	Ile	Val	Arg	Arg
65					70					75				80	
Asn	Ile	Thr	Asp	Arg	Ile	Trp	Leu	Ala	Ser	Glu	Ala	Trp	Ala	Ser	Ser
				85					90					95	
Ser	Leu	Ile	Ala	Lys	Pro	Glu	Tyr	Phe	His	Val	Val	Gly	Gly	Thr	Ile
			100					105					110		
Gly	Phe	Ala	Leu	Arg	Ala	Gly	Arg	Ile	Pro	Gly	Phe	His	Glu	Phe	Leu
		115					120					125			
Lys	Lys	Val	His	Pro	Ser	Arg	Ser	Ser	His	Asn	Gly	Phe	Val	Lys	Glu
	130					135					140				
Phe	Trp	Glu	Glu	Thr	Phe	Asn	Cys	Tyr	Phe	Thr	Glu	Glu	Ser	Leu	Thr
145					150					155					160
Gln	Leu	Lys	Asn	Cys	Lys	Thr	Pro	Thr	His	Gly	Leu	Ala	Met	His	Asn
				165					170					175	
Asp	Ser	Ala	Lys	Met	Gly	His	Ser	Thr	Arg	Thr	Thr	Leu	Arg	Pro	Pro
			180					185					190		
Cys	Thr	Gly	Glu	Glu	Asn	Ile	Thr	Ser	Val	Glu	Thr	Pro	Tyr	Leu	Asp
		195					200					205			
Tyr	Thr	His	Leu	Arg	Ile	Ser	Tyr	Asn	Val	Tyr	Val	Ala	Val	Tyr	Ser
	210					215					220				
Ile	Ala	His	Ala	Leu	Gln	Asp	Ile	Tyr	Ala	Cys	Thr	Pro	Gly	Lys	Gly
225					230					235					240
Ile	Phe	Ala	Asn	Gly	Ser	Cys	Ala	Asp	Ile	Lys	Lys	Val	Glu	Ala	Trp
				245					250					255	
Asn	Pro	Tyr	Asp												
			260												

Polypeptide SEQ ID NO: 4

Annotated Sheet

Polynucleotide SEQ ID NO: 3; Polypeptide SEQ ID NO: 4

10 20 30 40 50
* * * * *
CTA CTA GTC ATA TGG ATT GCG GCG GAY GAY GAT TAT GGC CGC CCA GGG ATA GAT
GAT GAT CAG TAT ACC TAA CGC CGC CTR CTR CTA ATA CCG GCG GGT CCC TAT CTA
Leu Leu Val Ile Trp Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Asp>
_ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ ORF RF[1] _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ >

60 70 80 90 100
* * * * *
AAG TTT CGA GAA GAA GCT GAA GAG AGG GAC ATC TGC ATA GAT TTC AAT GAG ATG
TTC AAA GCT CTT CTT CGA CTT CTC TCC CTG TAG ACG TAT CTA AAG TTA CTC TAC
Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp Phe Asn Glu Met>
_ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ ORF RF[1] _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ >

110 120 130 140 150 160
* * * * *
ATT TCT CAG TAC TAT ACA CAA AAA GAG CTG GAG TTT ATT GCA GAT ACT ATT CAG
TAA AGA GTC ATG ATA TGT GTT TTT CTC GAC CTC AAA TAA CGT CTA TGA TAA GTC
Ile Ser Gln Tyr Tyr Thr Gln Lys Glu Leu Glu Phe Ile Ala Asp Thr Ile Gln>
_ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ ORF RF[1] _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ >

170 180 190 200 210
* * * * *
AAT TCC TCA GCC AAA GTG ATT GTY GTC TTC TCA AAT GGC CCT GAC TTG GAA CCA
TTA AGG AGT CGG TTT CAC TAA CAA CAG AAG AGT TTA CCG GGA CTG AAC CTT GGT
Asn Ser Ser Ala Lys Val Ile Val Val Phe Ser Asn Gly Pro Asp Leu Glu Pro>
_ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ ORF RF[1] _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ >

220 230 240 250 260 270
* * * * *
CTA ATA CAA GAG ATA GTT CGA CGG AAC ATA ACT GAT AGA ATA TGG CTA GCA AGT
GAT TAT GTT CTC TAT CAA GCT GCC TTG TAT TGA CTA TCT TAT ACC GAT CGT TCA
Leu Ile Gln Glu Ile Val Arg Arg Asn Ile Thr Asp Arg Ile Trp Leu Ala Ser>
_ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ ORF RF[1] _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ >

280 290 300 310 320
* * * * *
GAA GCG TGG GCT AGT TCC TCA CTG ATA GCC AAA CCA GAA TAC TTC CAT GTT GTT
CTT CGC ACC CGA TCA AGG AGT GAC TAT CGG TTT GGT CTT ATG AAG GTA CAA CAA
Glu Ala Trp Ala Ser Ser Ser Leu Ile Ala Lys Pro Glu Tyr Phe His Val Val>
_ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ ORF RF[1] _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ >

330 340 350 360 370
* * * * *
GGT GGA ACC ATT GGA TTT GCA CTA AGA GCA GGA CGC ATC CCA GGA TTC CAT GAG
CCA CCT TGG TAA CCT AAA CGT GAT TCT CGT CCT CGC TAG GGT CCT AAG GTA CTC
Gly Gly Thr Ile Gly Phe Ala Leu Arg Ala Gly Arg Ile Pro Gly Phe His Glu>
_ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ ORF RF[1] _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ >

380 390 400 410 420 430
* * * * *
TTT TTA AAA AAG GTC CAT CCC AGC AGG TCC TCC CAC AAT GGC TTT GTC AAG GAA
AAA AAT TTT TTC CAG GTA GGG TCG TCC AGG AGG GTG TTA CCG AAA CAG TTC CTT
Phe Leu Lys Lys Val His Pro Ser Arg Ser Ser His Asn Gly Phe Val Lys Glu>
_ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ ORF RF[1] _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ >

440 450 460 470 480
* * * * *
TTC TGG GAA GAA ACA TTT AAT TGT TAT TTC ACT GAA GAA TCC CTA ACA CAA CTA
AAG ACC CTT CTT TGT AAA TTA ACA ATA AAG TGA CTT CTT AGG GAT TGT GTT GAT
Phe Trp Glu Glu Thr Phe Asn Cys Tyr Phe Thr Glu Glu Ser Leu Thr Gln Leu>
_ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ ORF RF[1] _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ a _ _ _ _ _ >

FIG. 18A

Polynucleotide SEQ ID NO: 3; Polypeptide SEQ ID NO: 4 (CONTINUED)

490 *	500 *	510 *	520 *	530 *	540 *
AAG AAT TGC AAA ACA CCA ACC CAT GGA TTA	GCA ATG CAC AAT GAC AGT GCG AAA	TTC TTA ACG TTT TGT GGT TGG GTA CCT AAT	CGT TAC GTG TTA CTG TCA CGC TTT	Lys Asn Cys Lys Thr Pro Thr His Gly Leu	Ala Met His Asn Asp Ser Ala Lys>
___a___a___a___a___a___a___a___ORF RF[1] ___a___a___a___a___a___a___a___>					
550 *	560 *	570 *	580 *	590 *	
ATG GGG CAT TCC ACA AGG ACA ACG TTA CGA	CCT CCA TGC ACT GGA GAA GAG AAT	TAC CCC GTA AGG TGT TCC TGT TGC AAT GCT	GGA GGT ACG TGA CCT CTT CTC TTA	Met Gly His Ser Thr Arg Thr Thr Leu Arg	Pro Pro Cys Thr Gly Glu Glu Asn>
___a___a___a___a___a___a___a___ORF RF[1] ___a___a___a___a___a___a___a___>					
600 *	610 *	620 *	630 *	640 *	
ATC ACG AGT GTG GAG ACC CCT TAC CTG GAT	TAT ACT CAC CTC CGT ATT TCA TAT	TAG TGC TCA CAC CTC TGG GGA ATG GAC CTA	ATA TGA GTG GAG GCA TAA AGT ATA	Ile Thr Ser Val Glu Thr Pro Tyr Leu Asp	Tyr Thr His Leu Arg Ile Ser Tyr>
___a___a___a___a___a___a___a___ORF RF[1] ___a___a___a___a___a___a___a___>					
650 *	660 *	670 *	680 *	690 *	700 *
AAT GTG TAT GTG GCA GTG TAT TCG ATT GCT	CAC GCT CTG CAG GAC ATC TAT GCC	TTA CAC ATA CAC CGT CAC ATA AGC TAA CGA	GTG CGA GAC GTC CTG TAG ATA CGG	Asn Val Tyr Val Ala Val Tyr Ser Ile Ala	His Ala Leu Gln Asp Ile Tyr Ala>
___a___a___a___a___a___a___a___ORF RF[1] ___a___a___a___a___a___a___a___>					
710 *	720 *	730 *	740 *	750 *	
TGC ACA CCT GGG AAG GGG ATT TTT GCG AAC	GGA TCA TGT GCC GAT ATC AAA AAA	ACG TGT GGA CCC TTC CCC TAA AAA CGC TTG	CCT AGT ACA CGG CTA TAG TTT TTT	Cys Thr Pro Gly Lys Gly Ile Phe Ala Asn	Gly Ser Cys Ala Asp Ile Lys Lys>
___a___a___a___a___a___a___a___ORF RF[1] ___a___a___a___a___a___a___a___>					
760 *	770 *	780 *			
GTC GAA GCC TGG AAT CCA TAT GAC TAGT	CAG CTT CGG ACC TTA GGT ATA CTG ATCA	Val Glu Ala Trp Asn Pro Tyr Asp>			
___a___a___a___a___a___a___a___ORF RF[1] ___a___a___a___a___a___a___a___>					

tt ctg aca ata ttt gct gtg cta gga ata ctg atc act tcc ttt gtt	47
Leu Thr Ile Phe Ala Val Leu Gly Ile Leu Ile Thr Ser Phe Val	
1 5 10 15	
ttg gga gta ttc att aag ttc aga aat act cct att gtg aaa gcc act	95
Leu Gly Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val Lys Ala Thr	
20 25 30	
aac aga gaa ctc tcc tat ctc ctc ctc ttc tcc tta atc tgc tgt ttc	143
Asn Arg Glu Leu Ser Tyr Leu Leu Phe Ser Leu Ile Cys Cys Phe	
35 40 45	
tcc agc tca ttg atc ttc att gga gaa ccc aaa gat tgg acc tgc aga	191
Ser Ser Ser Leu Ile Phe Ile Gly Glu Pro Lys Asp Trp Thr Cys Arg	
50 55 60	
ctg cgt caa cct gca ttt gga atc agc ttt gtg ctg tgc att tct tgc	239
Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys	
65 70 75	
att ctg gtg aaa act aat cgt gtg cta ttg gtc ttt gag gcc aag atc	287
Ile Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu Ala Lys Ile	
80 85 90 95	
cca act agc ctc cat cga aag tgg gtg ggc ctc aat ttg caa ttc tta	335
Pro Thr Ser Leu His Arg Lys Trp Val Gly Leu Asn Leu Gln Phe Leu	
100 105 110	
ctg gtt ttc ctc tgt att ctt gtg caa att gtt act tgt gtc atc tgg	383
Leu Val Phe Leu Cys Ile Leu Val Gln Ile Val Thr Cys Val Ile Trp	
115 120 125	
ctt tac aca gca ccc cct tcg agc tac aga aat cat gaa cta gaa gat	431
Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg Asn His Glu Leu Glu Asp	
130 135 140	
gaa atc att ttt att aca tgt gat gaa ggt tcc tta atg gca ctt ggt	479
Glu Ile Ile Phe Ile Thr Cys Asp Glu Gly Ser Leu Met Ala Leu Gly	
145 150 155	
ttt ctc att ggt tac aca tgc ctc ctt gct gcc att tgc ttc ttt ttt	527
Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe	
160 165 170 175	
gcc ttt aag tct cgc aaa ctc cca gag aac ttc aat gag gcc aaa ttt	575
Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala Lys Phe	
180 185 190	
att acc ttc agc atg ctg ata tt	598
Ile Thr Phe Ser Met Leu Ile	
195	

Polynucleotide SEQ ID NO: 5; Polypeptide SEQ ID NO: 6

Leu	Thr	Ile	Phe	Ala	Val	Leu	Gly	Ile	Leu	Ile	Thr	Ser	Phe	Val	Leu
1				5					10					15	
Gly	Val	Phe	Ile	Lys	Phe	Arg	Asn	Thr	Pro	Ile	Val	Lys	Ala	Thr	Asn
			20					25					30		
Arg	Glu	Leu	Ser	Tyr	Leu	Leu	Leu	Phe	Ser	Leu	Ile	Cys	Cys	Phe	Ser
		35					40					45			
Ser	Ser	Leu	Ile	Phe	Ile	Gly	Glu	Pro	Lys	Asp	Trp	Thr	Cys	Arg	Leu
	50					55					60				
Arg	Gln	Pro	Ala	Phe	Gly	Ile	Ser	Phe	Val	Leu	Cys	Ile	Ser	Cys	Ile
65					70					75					80
Leu	Val	Lys	Thr	Asn	Arg	Val	Leu	Leu	Val	Phe	Glu	Ala	Lys	Ile	Pro
				85					90					95	
Thr	Ser	Leu	His	Arg	Lys	Trp	Val	Gly	Leu	Asn	Leu	Gln	Phe	Leu	Leu
			100					105					110		
Val	Phe	Leu	Cys	Ile	Leu	Val	Gln	Ile	Val	Thr	Cys	Val	Ile	Trp	Leu
		115					120					125			
Tyr	Thr	Ala	Pro	Pro	Ser	Ser	Tyr	Arg	Asn	His	Glu	Leu	Glu	Asp	Glu
	130					135					140				
Ile	Ile	Phe	Ile	Thr	Cys	Asp	Glu	Gly	Ser	Leu	Met	Ala	Leu	Gly	Phe
145					150					155					160
Leu	Ile	Gly	Tyr	Thr	Cys	Leu	Leu	Ala	Ala	Ile	Cys	Phe	Phe	Phe	Ala
				165					170					175	
Phe	Lys	Ser	Arg	Lys	Leu	Pro	Glu	Asn	Phe	Asn	Glu	Ala	Lys	Phe	Ile
			180					185					190		
Thr	Phe	Ser	Met	Leu	Ile										
		195													

Polypeptide SEQ ID NO: 6

FIG. 21A

Polynucleotide SEQ ID NO: 5; Polypeptide SEQ ID NO: 6 (CONTINUED)

```

      490          500          510          520          530
      *           *           *           *           *
ATT GGT TAC ACA TGC CTC CTT GCT GCC ATT TGC TTC TTT TTT GCC TTT AAG TCT
TAA CCA ATG TGT ACG GAG GAA CGA CGG TAA ACG AAG AAA AAA CGG AAA TTC AGA
Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe Ala Phe Lys Ser>
___a___a___a___a___a___a___a___a___a___a___a___a___a___a___a___a___>

540          550          560          570          580          590
*           *           *           *           *           *
CGC AAA CTC CCA GAG AAC TTC AAT GAG GCC AAA TTT ATT ACC TTC AGC ATG CTG
GCG TTT GAG GGT CTC TTG AAG TTA CTC CGG TTT AAA TAA TGG AAG TCG TAC GAC
Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala Lys Phe Ile Thr Phe Ser Met Leu>
___a___a___a___a___a___a___a___a___a___a___a___a___a___a___a___a___>

ATA TT
TAT AA
Ile>
___>
```

Polynucleotide SEQ ID NO: 7; Polypeptide SEQ ID NO: 8

g	ttg	acc	ata	tgt	gca	gtg	ctg	ggt	ggt	gcc	ytg	acg	ggc	ttc	gtg	atg	49
Leu	Thr	Ile	Cys	Ala	Val	Leu	Gly	Val	Ala	Xaa	Thr	Gly	Phe	Val	Met		
1				5					10					15			
gcc	gtc	ttt	gtc	cga	ttc	cgc	aac	acc	cca	ata	gtg	aaa	gcc	acg	aac	97	
Ala	Val	Phe	Val	Arg	Phe	Arg	Asn	Thr	Pro	Ile	Val	Lys	Ala	Thr	Asn		
			20					25					30				
cga	gaa	ctg	tcc	tac	gtc	ctc	ctg	ttc	tct	ctc	atc	tgt	tgc	ttc	tcc	145	
Arg	Glu	Leu	Ser	Tyr	Val	Leu	Leu	Phe	Ser	Leu	Ile	Cys	Cys	Phe	Ser		
		35					40					45					
agc	tcc	ctc	atc	ttc	ata	gga	gag	ccg	cag	gat	tgg	atg	tgc	cgc	tta	193	
Ser	Ser	Leu	Ile	Phe	Ile	Gly	Glu	Pro	Gln	Asp	Trp	Met	Cys	Arg	Leu		
	50					55				60							
cgc	caa	ccg	gcc	ttt	ggg	atc	agt	ttt	gtt	ctc	tgt	atc	tcg	tgc	atc	241	
Arg	Gln	Pro	Ala	Phe	Gly	Ile	Ser	Phe	Val	Leu	Cys	Ile	Ser	Cys	Ile		
65					70				75						80		
ctt	gtg	aaa	aca	aac	cka	gtc	ctc	ttg	gtg	ttt	gaa	gcc	aag	atc	ccg	289	
Leu	Val	Lys	Thr	Asn	Xaa	Val	Leu	Leu	Val	Phe	Glu	Ala	Lys	Ile	Pro		
				85					90					95			
aca	agt	ctc	cat	cgt	aaa	tgg	tgg	ggg	tta	aac	cta	cag	ttc	ctg	ctg	337	
Thr	Ser	Leu	His	Arg	Lys	Trp	Trp	Gly	Leu	Asn	Leu	Gln	Phe	Leu	Leu		
			100					105					110				
gtg	ttt	ctg	tgc	aca	ttt	gtc	caa	gtc	atg	ata	tgt	gtg	gtc	tgg	ctg	385	
Val	Phe	Leu	Cys	Thr	Phe	Val	Gln	Val	Met	Ile	Cys	Val	Val	Trp	Leu		
		115					120					125					
tac	aac	gcc	cca	cct	tcc	agt	tac	agg	aat	tat	gac	ata	gat	gag	atg	433	
Tyr	Asn	Ala	Pro	Pro	Ser	Ser	Tyr	Arg	Asn	Tyr	Asp	Ile	Asp	Glu	Met		
	130					135					140						
att	ttt	atc	aca	tgt	aat	gaa	ggc	tct	gta	atg	gct	ctt	ggg	ttt	ctt	481	
Ile	Phe	Ile	Thr	Cys	Asn	Glu	Gly	Ser	Val	Met	Ala	Leu	Gly	Phe	Leu		
145					150					155					160		
att	ggc	tat	aca	tgc	ctg	ctg	gcc	gct	ata	tgt	ttc	ttc	ttt	gca	ttc	529	
Ile	Gly	Tyr	Thr	Cys	Leu	Leu	Ala	Ala	Ile	Cys	Phe	Phe	Phe	Ala	Phe		
				165				170						175			
aaa	tca	cgg	aaa	ctt	cca	gaa	aac	ttc	acc	gag	gct	aag	ttc	atc	act	577	
Lys	Ser	Arg	Lys	Leu	Pro	Glu	Asn	Phe	Thr	Glu	Ala	Lys	Phe	Ile	Thr		
			180					185					190				
ttt	agt	atg	ctc	ata	tt											594	
Phe	Ser	Met	Leu	Ile													
			195														

Leu	Thr	Ile	Cys	Ala	Val	Leu	Gly	Val	Ala	Leu	Thr	Gly	Phe	Val	Met
1				5					10					15	
Ala	Val	Phe	Val	Arg	Phe	Arg	Asn	Thr	Pro	Ile	Val	Lys	Ala	Thr	Asn
			20					25					30		
Arg	Glu	Leu	Ser	Tyr	Val	Leu	Leu	Phe	Ser	Leu	Ile	Cys	Cys	Phe	Ser
		35					40					45			
Ser	Ser	Leu	Ile	Phe	Ile	Gly	Glu	Pro	Gln	Asp	Trp	Met	Cys	Arg	Leu
	50					55					60				
Arg	Gln	Pro	Ala	Phe	Gly	Ile	Ser	Phe	Val	Leu	Cys	Ile	Ser	Cys	Ile
65					70					75					80
Leu	Val	Lys	Thr	Asn	Xaa	Val	Leu	Leu	Val	Phe	Glu	Ala	Lys	Ile	Pro
				85					90					95	
Thr	Ser	Leu	His	Arg	Lys	Trp	Trp	Gly	Leu	Asn	Leu	Gln	Phe	Leu	Leu
			100					105					110		
Val	Phe	Leu	Cys	Thr	Phe	Val	Gln	Val	Met	Ile	Cys	Val	Val	Trp	Leu
		115					120					125			
Tyr	Asn	Ala	Pro	Pro	Ser	Ser	Tyr	Arg	Asn	Tyr	Asp	Ile	Asp	Glu	Met
	130					135					140				
Ile	Phe	Ile	Thr	Cys	Asn	Glu	Gly	Ser	Val	Met	Ala	Leu	Gly	Phe	Leu
145					150					155					160
Ile	Gly	Tyr	Thr	Cys	Leu	Leu	Ala	Ala	Ile	Cys	Phe	Phe	Phe	Ala	Phe
				165					170					175	
Lys	Ser	Arg	Lys	Leu	Pro	Glu	Asn	Phe	Thr	Glu	Ala	Lys	Phe	Ile	Thr
			180					185					190		
Phe	Ser	Met	Leu	Ile											
		195													

Polypeptide SEQ ID NO: 8

Polynucleotide SEQ ID NO: 7; Polypeptide SEQ ID NO: 8

FIG. 24A

FIG. 24B

tg	tcg	tgg	acg	gag	ccc	ttt	ggg	atc	gcg	ttg	gcc	ata	tgt	gca	gcg	47
Ser	Trp	Thr	Glu	Pro	Phe	Gly	Ile	Ala	Leu	Ala	Ile	Cys	Ala	Ala		
1				5					10					15		
ctg	ggg	gtt	gcc	ttg	acg	ggc	ttc	gtg	atg	gcc	gtc	ttt	atc	aga	ttc	95
Leu	Gly	Val	Ala	Leu	Thr	Gly	Phe	Val	Met	Ala	Val	Phe	Ile	Arg	Phe	
			20					25						30		
cgc	aac	acc	cca	ata	gtg	aag	gcc	acg	aac	cga	gaa	ctg	tcc	tat	gtc	143
Arg	Asn	Thr	Pro	Ile	Val	Lys	Ala	Thr	Asn	Arg	Glu	Leu	Ser	Tyr	Val	
			35				40						45			
ctc	ctg	ttc	tct	ctc	atc	tgt	tgc	ttc	tcc	agt	tcc	ctc	atc	ttt	att	191
Leu	Leu	Phe	Ser	Leu	Ile	Cys	Cys	Phe	Ser	Ser	Ser	Leu	Ile	Phe	Ile	
		50					55					60				
gga	gag	ccg	cag	gat	tgg	atg	tgt	cgt	tta	cgc	caa	cct	gcc	ttt	ggg	239
Gly	Glu	Pro	Gln	Asp	Trp	Met	Cys	Arg	Leu	Arg	Gln	Pro	Ala	Phe	Gly	
	65					70					75					
atc	agt	ttt	gtt	ctc	tgt	atc	tcc	tgc	atc	ctt	gtg	aaa	act	aat	aga	287
Ile	Ser	Phe	Val	Leu	Cys	Ile	Ser	Cys	Ile	Leu	Val	Lys	Thr	Asn	Arg	
80					85					90					95	
gta	ctc	tta	gta	ttt	gaa	gcc	aag	atc	ccc	aca	agt	ctc	cat	cgt	aaa	335
Val	Leu	Leu	Val	Phe	Glu	Ala	Lys	Ile	Pro	Thr	Ser	Leu	His	Arg	Lys	
			100						105					110		
tgg	tgg	ggg	tta	aac	ctt	cag	ttt	ttg	ctg	gtg	ttt	ctg	tgc	aca	ttt	383
Trp	Trp	Gly	Leu	Asn	Leu	Gln	Phe	Leu	Leu	Val	Phe	Leu	Cys	Thr	Phe	
			115					120					125			
gtc	caa	gtc	atg	atc	tgt	gtt	gtc	tgg	ctg	tac	aat	gcc	cct	ccc	tcc	431
Val	Gln	Val	Met	Ile	Cys	Val	Val	Trp	Leu	Tyr	Asn	Ala	Pro	Pro	Ser	
		130					135					140				
agt	tac	agg	aat	tat	gac	ata	gat	gag	atg	att	ttt	atc	aca			473
Ser	Tyr	Arg	Asn	Tyr	Asp	Ile	Asp	Glu	Met	Ile	Phe	Ile	Thr			
	145					150					155					
tg																475

Polynucleotide SEQ ID NO: 9; Polypeptide SEQ ID NO: 10

Ser	Trp	Thr	Glu	Pro	Phe	Gly	Ile	Ala	Leu	Ala	Ile	Cys	Ala	Ala	Leu
1				5					10					15	
Gly	Val	Ala	Leu	Thr	Gly	Phe	Val	Met	Ala	Val	Phe	Ile	Arg	Phe	Arg
			20					25					30		
Asn	Thr	Pro	Ile	Val	Lys	Ala	Thr	Asn	Arg	Glu	Leu	Ser	Tyr	Val	Leu
		35					40					45			
Leu	Phe	Ser	Leu	Ile	Cys	Cys	Phe	Ser	Ser	Ser	Leu	Ile	Phe	Ile	Gly
	50					55					60				
Glu	Pro	Gln	Asp	Trp	Met	Cys	Arg	Leu	Arg	Gln	Pro	Ala	Phe	Gly	Ile
65					70					75					80
Ser	Phe	Val	Leu	Cys	Ile	Ser	Cys	Ile	Leu	Val	Lys	Thr	Asn	Arg	Val
				85					90					95	
Leu	Leu	Val	Phe	Glu	Ala	Lys	Ile	Pro	Thr	Ser	Leu	His	Arg	Lys	Trp
			100					105					110		
Trp	Gly	Leu	Asn	Leu	Gln	Phe	Leu	Leu	Val	Phe	Leu	Cys	Thr	Phe	Val
		115					120					125			
Gln	Val	Met	Ile	Cys	Val	Val	Trp	Leu	Tyr	Asn	Ala	Pro	Pro	Ser	Ser
	130					135					140				
Tyr	Arg	Asn	Tyr	Asp	Ile	Asp	Glu	Met	Ile	Phe	Ile	Thr			
145					150					155					

Polypeptide SEQ ID NO: 10

	10	20	30	40	50
TG TCG TGG ACG GAG CCC TTT GGG ATC GCG TTG GCC ATA TGT GCA GCG CTG GGT AC AGC ACC TGC CTC GGG AAA CCC TAG CGC AAC CGG TAT ACA CGT CGC GAC CCA Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu Ala Ile Cys Ala Ala Leu Gly> _ _ _ _ _ ORF RF[3] _ _ _ _ _					
	60	70	80	90	100
GTT GCC TTG ACG GGC TTC GTG ATG GCC GTC TTT ATC AGA TTC CGC AAC ACC CCA CAA CGG AAC TGC CCG AAG CAC TAC CGG CAG AAA TAG TCT AAG GCG TTG TGG GGT Val Ala Leu Thr Gly Phe Val Met Ala Val Phe Ile Arg Phe Arg Asn Thr Pro> _ _ _ _ _ ORF RF[3] _ _ _ _ _					
110	120	130	140	150	160
ATA GTG AAG GCC ACG AAC CGA GAA CTG TCC TAT GTC CTC CTG TTC TCT CTC ATC TAT CAC TTC CGG TGC TTG GCT CTT GAC AGG ATA CAG GAG GAC AAG AGA GAG TAG Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Val Leu Leu Phe Ser Leu Ile> _ _ _ _ _ ORF RF[3] _ _ _ _ _					
	170	180	190	200	210
TGT TGC TTC TCC AGT TCC CTC ATC TTT ATT GGA GAG CCG CAG GAT TGG ATG TGT ACA ACG AAG AGG TCA AGG GAG TAG AAA TAA CCT CTC GGC GTC CTA ACC TAC ACA Cys Cys Phe Ser Ser Ser Leu Ile Phe Ile Gly Glu Pro Gln Asp Trp Met Cys> _ _ _ _ _ ORF RF[3] _ _ _ _ _					
220	230	240	250	260	
CGT TTA CGC CAA CCT GCC TTT GGG ATC AGT TTT GTT CTC TGT ATC TCC TGC ATC GCA AAT GCG GTT GGA CGG AAA CCC TAG TCA AAA CAA GAG ACA TAG AGG ACG TAG Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys Ile> _ _ _ _ _ ORF RF[3] _ _ _ _ _					
270	280	290	300	310	320
CTT GTG AAA ACT AAT AGA GTA CTC TTA GTA TTT GAA GCC AAG ATC CCC ACA AGT GAA CAC TTT TGA TTA TCT CAT GAG AAT CAT AAA CTT CGG TTC TAG GGG TGT TCA Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu Ala Lys Ile Pro Thr Ser> _ _ _ _ _ ORF RF[3] _ _ _ _ _					
	330	340	350	360	370
CTC CAT CGT AAA TGG TGG GGG TTA AAC CTT CAG TTT TTG CTG GTG TTT CTG TGC GAG GTA GCA TTT ACC ACC CCC AAT TTG GAA GTC AAA AAC GAC CAC AAA GAC ACG Leu His Arg Lys Trp Trp Gly Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys> _ _ _ _ _ ORF RF[3] _ _ _ _ _					
380	390	400	410	420	430
ACA TTT GTC CAA GTC ATG ATC TGT GTT GTC TGG CTG TAC AAT GCC CCT CCC TCC TGT AAA CAG GTT CAG TAC TAG ACA CAA CAG ACC GAC ATG TTA CGG GGA GGG AGG Thr Phe Val Gln Val Met Ile Cys Val Val Trp Leu Tyr Asn Ala Pro Pro Ser> _ _ _ _ _ ORF RF[3] _ _ _ _ _					
	440	450	460	470	
AGT TAC AGG AAT TAT GAC ATA GAT GAG ATG ATT TTT ATC ACA TG TCA ATG TCC TTA ATA CTG TAT CTA CTC TAC TAA AAA TAG TGT AC Ser Tyr Arg Asn Tyr Asp Ile Asp Glu Met Ile Phe Ile Thr> _ _ _ _ _ ORF RF[3] _ _ _ _ _					

FIG. 27

Polynucleotide SEQ ID NO: 11; Polypeptide SEQ ID NO: 12

a	cgc	cca	ggg	att	gaa	aaa	ttt	gag	aag	gag	atg	gag	gag	cga	gac	atc	49
	Arg	Pro	Gly	Ile	Glu	Lys	Phe	Glu	Lys	Glu	Met	Glu	Glu	Arg	Asp	Ile	
	1				5					10					15		
tgc	att	cac	ctt	aat	gaa	ctt	atc	tct	cag	tat	ttt	gag	gag	cat	gaa	97	
Cys	Ile	His	Leu	Asn	Glu	Leu	Ile	Ser	Gln	Tyr	Phe	Glu	Asp	His	Glu		
			20					25					30				
atc	caa	gcg	ctg	gct	gac	agg	att	gag	aac	tcc	aca	gct	aaa	gtc	atc	145	
Ile	Gln	Ala	Leu	Ala	Asp	Arg	Ile	Glu	Asn	Ser	Thr	Ala	Lys	Val	Ile		
		35					40					45					
gta	gtg	ttt	gcc	agc	ggc	cca	gat	atc	gag	cct	tta	atc	aaa	gag	atg	193	
Val	Val	Phe	Ala	Ser	Gly	Pro	Asp	Ile	Glu	Pro	Leu	Ile	Lys	Glu	Met		
	50					55					60						
gtg	agg	aga	aac	atc	aca	gac	cgt	atc	tgg	tta	gcc	agt	gaa	gcg	tgg	241	
Val	Arg	Arg	Asn	Ile	Thr	Asp	Arg	Ile	Trp	Leu	Ala	Ser	Glu	Ala	Trp		
	65				70				75					80			
gct	agc	tcc	tct	ctt	ata	gct	aaa	cca	gag	tat	ctt	gat	ggt	gtg	gct	289	
Ala	Ser	Ser	Ser	Leu	Ile	Ala	Lys	Pro	Glu	Tyr	Leu	Asp	Val	Val	Ala		
				85					90					95			
ggg	act	atc	ggc	ttt	gct	ctc	aag	gca	ggg	cat	att	cct	ggc	tta	aga	337	
Gly	Thr	Ile	Gly	Phe	Ala	Leu	Lys	Ala	Gly	His	Ile	Pro	Gly	Leu	Arg		
			100					105					110				
gag	ttc	cta	cag	caa	gtg	caa	cca	aag	aga	gac	agt	cat	aat	gaa	ttt	385	
Glu	Phe	Leu	Gln	Gln	Val	Gln	Pro	Lys	Arg	Asp	Ser	His	Asn	Glu	Phe		
		115					120					125					
gtc	agg	gag	ttt	tgg	gaa	gaa	acc	ttc	aac	tgt	tat	ctg	gaa	gac	agc	433	
Val	Arg	Glu	Phe	Trp	Glu	Glu	Thr	Phe	Asn	Cys	Tyr	Leu	Glu	Asp	Ser		
	130					135					140						
cag	aga	cag	cag	gaa	agt	gag	aat	ggc	agc	aca	agt	ttc	agg	cct	ttg	481	
Gln	Arg	Gln	Gln	Glu	Ser	Glu	Asn	Gly	Ser	Thr	Ser	Phe	Arg	Pro	Leu		
	145				150				155						160		
tgt	act	ggt	gag	gaa	gac	atc	aca	agt	ggt	gag	acc	ccg	tac	ttg	gac	529	
Cys	Thr	Gly	Glu	Glu	Asp	Ile	Thr	Ser	Val	Glu	Thr	Pro	Tyr	Leu	Asp		
			165					170						175			
tac	aca	cac	ttt	cgt	atc	tcc	tat	aac	gtg	tat	ggt	gca	ggt	tat	tcc	577	
Tyr	Thr	His	Phe	Arg	Ile	Ser	Tyr	Asn	Val	Tyr	Val	Ala	Val	Tyr	Ser		
			180					185					190				
att	gca	cag	gcc	ctg	cag	gac	ata	ctc	acc	tgc	aca	cct	gga	cat	gga	625	
Ile	Ala	Gln	Ala	Leu	Gln	Asp	Ile	Leu	Thr	Cys	Thr	Pro	Gly	His	Gly		
		195				200						205					
ctc	ttt	gcc	aac	aat	tcc	tgt	gcc	gat	ata	aag	aaa	atg	gaa	gca	tgg	673	
Leu	Phe	Ala	Asn	Asn	Ser	Cys	Ala	Asp	Ile	Lys	Lys	Met	Glu	Ala	Trp		
	210					215						220					

Polynucleotide SEQ ID NO: 11; Polypeptide SEQ ID NO: 12 (CONTINUED)

cag gcc ctg aag cag ctt-aga cat ttg aac tac acc aac agc atg ggg Gln Ala Leu Lys Gln Leu Arg His Leu Asn Tyr Thr Asn Ser Met Gly 225 230 235 240	721
gaa aag atg cac ttt gat gag aac tca gac atg gca tca aac tac acc Glu Lys Met His Phe Asp Glu Asn Ser Asp Met Ala Ser Asn Tyr Thr 245 250 255	769
att ata aac tgg cac cgg tct gct gag gat ggc tct gtg gtg ttt gag Ile Ile Asn Trp His Arg Ser Ala Glu Asp Gly Ser Val Val Phe Glu 260 265 270	817
gac gtg gga tac tac agc atg cac gtc aag aga gga gcc aaa ctg ttc Asp Val Gly Tyr Tyr Ser Met His Val Lys Arg Gly Ala Lys Leu Phe 275 280 285	865
att gac aag aca aag att ttg tgg aat gga tac agt tgg gag gcg cca Ile Asp Lys Thr Lys Ile Leu Trp Asn Gly Tyr Ser Ser Glu Ala Pro 290 295 300	913
ttc tct aat tgc agt gag gac tgt gaa cct ggt aca agg aag ggg atc Phe Ser Asn Cys Ser Glu Asp Cys Glu Pro Gly Thr Arg Lys Gly Ile 305 310 315 320	961
att gac agt atg ccc aca tgt tgc ttt gaa tgc act gag tgc tca gat Ile Asp Ser Met Pro Thr Cys Cys Phe Glu Cys Thr Glu Cys Ser Asp 325 330 335	1009
gga gag tac agt aat cat aaa gat gcc agt gtt tgc acc aag tgt cca Gly Glu Tyr Ser Asn His Lys Asp Ala Ser Val Cys Thr Lys Cys Pro 340 345 350	1057
tat aac tct tgg tcc aat ggg aat cac aca ttc tgc ttc ctg aag gaa Tyr Asn Ser Trp Ser Asn Gly Asn His Thr Phe Cys Phe Leu Lys Glu 355 360 365	1105
atc gag ttt ctc tcc tgg aca gaa cca ttc ggg ata gct ttg gcc ata Ile Glu Phe Leu Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu Ala Ile 370 375 380	1153
tgt gca gta ctg ggt gtg ctc ttg aca gct ttt gtg atc gga gtc ttt Cys Ala Val Leu Gly Val Leu Leu Thr Ala Phe Val Ile Gly Val Phe 385 390 395 400	1201
gtc aga ttc cgc aac acc cca ata gtg aag gcc aca aac cga gaa ctg Val Arg Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu 405 410 415	1249
tcc tac gtt ctc ctg twc tca ctt atc tgt tgc ttc tca agc tcc ctc Ser Tyr Val Leu Leu Xaa Ser Leu Ile Cys Cys Phe Ser Ser Ser Leu 420 425 430	1297
akc ttc atc gg Xaa Phe Ile 435	1308

Polypeptide SEQ ID NO: 12

Arg	Pro	Gly	Ile	Glu	Lys	Phe	Glu	Lys	Glu	Met	Glu	Glu	Arg	Asp	Ile
1				5					10					15	
Cys	Ile	His	Leu	Asn	Glu	Leu	Ile	Ser	Gln	Tyr	Phe	Glu	Asp	His	Glu
			20					25					30		
Ile	Gln	Ala	Leu	Ala	Asp	Arg	Ile	Glu	Asn	Ser	Thr	Ala	Lys	Val	Ile
		35				40						45			
Val	Val	Phe	Ala	Ser	Gly	Pro	Asp	Ile	Glu	Pro	Leu	Ile	Lys	Glu	Met
	50				55					60					
Val	Arg	Arg	Asn	Ile	Thr	Asp	Arg	Ile	Trp	Leu	Ala	Ser	Glu	Ala	Trp
65				70					75						80
Ala	Ser	Ser	Ser	Leu	Ile	Ala	Lys	Pro	Glu	Tyr	Leu	Asp	Val	Val	Ala
				85				90					95		
Gly	Thr	Ile	Gly	Phe	Ala	Leu	Lys	Ala	Gly	His	Ile	Pro	Gly	Leu	Arg
			100					105					110		
Glu	Phe	Leu	Gln	Gln	Val	Gln	Pro	Lys	Arg	Asp	Ser	His	Asn	Glu	Phe
		115				120						125			
Val	Arg	Glu	Phe	Trp	Glu	Glu	Thr	Phe	Asn	Cys	Tyr	Leu	Glu	Asp	Ser
	130				135						140				
Gln	Arg	Gln	Gln	Glu	Ser	Glu	Asn	Gly	Ser	Thr	Ser	Phe	Arg	Pro	Leu
145				150					155						160
Cys	Thr	Gly	Glu	Glu	Asp	Ile	Thr	Ser	Val	Glu	Thr	Pro	Tyr	Leu	Asp
				165				170						175	
Tyr	Thr	His	Phe	Arg	Ile	Ser	Tyr	Asn	Val	Tyr	Val	Ala	Val	Tyr	Ser
			180					185					190		
Ile	Ala	Gln	Ala	Leu	Gln	Asp	Ile	Leu	Thr	Cys	Thr	Pro	Gly	His	Gly
		195				200						205			
Leu	Phe	Ala	Asn	Asn	Ser	Cys	Ala	Asp	Ile	Lys	Lys	Met	Glu	Ala	Trp
	210					215					220				
Gln	Ala	Leu	Lys	Gln	Leu	Arg	His	Leu	Asn	Tyr	Thr	Asn	Ser	Met	Gly
225				230					235						240
Glu	Lys	Met	His	Phe	Asp	Glu	Asn	Ser	Asp	Met	Ala	Ser	Asn	Tyr	Thr
				245				250					255		
Ile	Ile	Asn	Trp	His	Arg	Ser	Ala	Glu	Asp	Gly	Ser	Val	Val	Phe	Glu
			260					265					270		
Asp	Val	Gly	Tyr	Tyr	Ser	Met	His	Val	Lys	Arg	Gly	Ala	Lys	Leu	Phe
		275				280						285			
Ile	Asp	Lys	Thr	Lys	Ile	Leu	Trp	Asn	Gly	Tyr	Ser	Ser	Glu	Ala	Pro
	290				295						300				
Phe	Ser	Asn	Cys	Ser	Glu	Asp	Cys	Glu	Pro	Gly	Thr	Arg	Lys	Gly	Ile
305				310						315					320
Ile	Asp	Ser	Met	Pro	Thr	Cys	Cys	Phe	Glu	Cys	Thr	Glu	Cys	Ser	Asp
				325				330					335		
Gly	Glu	Tyr	Ser	Asn	His	Lys	Asp	Ala	Ser	Val	Cys	Thr	Lys	Cys	Pro
			340					345					350		
Tyr	Asn	Ser	Trp	Ser	Asn	Gly	Asn	His	Thr	Phe	Cys	Phe	Leu	Lys	Glu
		355				360						365			
Ile	Glu	Phe	Leu	Ser	Trp	Thr	Glu	Pro	Phe	Gly	Ile	Ala	Leu	Ala	Ile
	370					375					380				
Cys	Ala	Val	Leu	Gly	Val	Leu	Leu	Thr	Ala	Phe	Val	Ile	Gly	Val	Phe
385				390						395					400
Val	Arg	Phe	Arg	Asn	Thr	Pro	Ile	Val	Lys	Ala	Thr	Asn	Arg	Glu	Leu
				405				410					415		
Ser	Tyr	Val	Leu	Xaa	Ser	Leu	Ile	Cys	Cys	Phe	Ser	Ser	Ser	Ser	Leu
			420				425					430			
Xaa	Phe	Ile													
		435													

Polynucleotide SEQ ID NO: 11; Polypeptide SEQ ID NO: 12 (CONTINUED)

490 * 500 * 510 * 520 * 530 *

ACT GGT GAG GAA GAC ATC ACA AGT GTT GAG ACC CCG TAC TTG GAC TAC ACA CAC
TGA CCA CTC CTT CTG TAG TGT TCA CAA CTC TGG GGC ATG AAC CTG ATG TGT GTG
Thr Gly Glu Glu Asp Ile Thr Ser Val Glu Thr Pro Tyr Leu Asp Tyr Thr His>
_ _ _ _ _ ORF RF[2] _ _ _ _ _

540 * 550 * 560 * 570 * 580 * 590 *

TTT CGT ATC TCC TAT AAC GTG TAT GTT GCA GTT TAT TCC ATT GCA CAG GCC CTG
AAA GCA TAG AGG ATA TTG CAC ATA CAA CGT CAA ATA AGG TAA CGT GTC CGG GAC
Phe Arg Ile Ser Tyr Asn Val Tyr Val Ala Val Tyr Ser Ile Ala Gln Ala Leu>
_ _ _ _ _ ORF RF[2] _ _ _ _ _

600 * 610 * 620 * 630 * 640 *

CAG GAC ATA CTC ACC TGC ACA CCT GGA CAT GGA CTC TTT GCC AAC AAT TCC TGT
GTC CTG TAT GAG TGG ACG TGT GGA CCT GTA CCT GAG AAA CGG TTG TTA AGG ACA
Gln Asp Ile Leu Thr Cys Thr Pro Gly His Gly Leu Phe Ala Asn Ser Cys>
_ _ _ _ _ ORF RF[2] _ _ _ _ _

650 * 660 * 670 * 680 * 690 * 700 *

GCC GAT ATA AAG AAA ATG GAA GCA TGG CAG GCC CTG AAG CAG CTT AGA CAT TTG
CGG CTA TAT TTC TTT TAC CTT CGT ACC GTC CGG GAC TTC GTC GAA TCT GTA AAC
Ala Asp Ile Lys Lys Met Glu Ala Trp Gln Ala Leu Lys Gln Leu Arg His Leu>
_ _ _ _ _ ORF RF[2] _ _ _ _ _

710 * 720 * 730 * 740 * 750 *

AAC TAC ACC AAC AGC ATG GGG GAA AAG ATG CAC TTT GAT GAG AAC TCA GAC ATG
TTG ATG TGG TTG TCG TAC CCC CTT TTC TAC GTG AAA CTA CTC TTG AGT CTG TAC
Asn Tyr Thr Asn Ser Met Gly Glu Lys Met His Phe Asp Glu Asn Ser Asp Met>
_ _ _ _ _ ORF RF[2] _ _ _ _ _

760 * 770 * 780 * 790 * 800 *

GCA TCA AAC TAC ACC ATT ATA AAC TGG CAC CGG TCT GCT GAG GAT GGC TCT GTG
CGT AGT TTG ATG TGG TAA TAT TTG ACC GTG GCC AGA CGA CTC CTA CCG AGA CAC
Ala Ser Asn Tyr Thr Ile Ile Asn Trp His Arg Ser Ala Glu Asp Gly Ser Val>
_ _ _ _ _ ORF RF[2] _ _ _ _ _

810 * 820 * 830 * 840 * 850 * 860 *

GTG TTT GAG GAC GTG GGA TAC TAC AGC ATG CAC GTC AAG AGA GGA GCC AAA CTG
CAC AAA CTC CTG CAC CCT ATG ATG TCG TAC GTG CAG TTC TCT CCT CGG TTT GAC
Val Phe Glu Asp Val Gly Tyr Tyr Ser Met His Val Lys Arg Gly Ala Lys Leu>
_ _ _ _ _ ORF RF[2] _ _ _ _ _

870 * 880 * 890 * 900 * 910 *

TTC ATT GAC AAG ACA AAG ATT TTG TGG AAT GGA TAC AGT TCG GAG GCG CCA TTC
AAG TAA CTG TTC TGT TTC TAA AAC ACC TTA CCT ATG TCA AGC CTC CGC GGT AAG
Phe Ile Asp Lys Thr Lys Ile Leu Trp Asn Gly Tyr Ser Ser Glu Ala Pro Phe>
_ _ _ _ _ ORF RF[2] _ _ _ _ _

920 * 930 * 940 * 950 * 960 * 970 *

TCT AAT TGC AGT GAG GAC TGT GAA CCT GGT ACA AGG AAG GGG ATC ATT GAC AGT
AGA TTA ACG TCA CTC CTG ACA CTT GGA CCA TGT TCC TTC CCC TAG TAA CTG TCA
Ser Asn Cys Ser Glu Asp Cys Glu Pro Gly Thr Arg Lys Gly Ile Ile Asp Ser>
_ _ _ _ _ ORF RF[2] _ _ _ _ _

FIG. 30B

Polynucleotide SEQ ID NO: 11; Polypeptide SEQ ID NO: 12 (CONTINUED)

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      980      990      1000      1010      1020
      *      *      *      *      *
ATG CCC ACA TGT TGC TTT GAA TGC ACT GAG TGC TCA GAT GGA GAG TAC AGT AAT
TAC GGG TGT ACA ACG AAA CTT ACG TGA CTC ACG AGT CTA CCT CTC ATG TCA TTA
Met Pro Thr Cys Cys Phe Glu Cys Thr Glu Cys Ser Asp Gly Glu Tyr Ser Asn>
___a___a___a___a___a___a___a___ORF RF[2] ___a___a___a___a___a___a___a___>

      1030      1040      1050      1060      1070
      *      *      *      *      *
CAT AAA GAT GCC AGT GTT TGC ACC AAG TGT CCA TAT AAC TCT TGG TCC AAT GGG
GTA TTT CTA CGG TCA CAA ACG TGG TTC ACA GGT ATA TTG AGA ACC AGG TTA CCC
His Lys Asp Ala Ser Val Cys Thr Lys Cys Pro Tyr Asn Ser Trp Ser Asn Gly>
___a___a___a___a___a___a___a___ORF RF[2] ___a___a___a___a___a___a___a___>

1080      1090      1100      1110      1120      1130
*      *      *      *      *      *
AAT CAC ACA TTC TGC TTC CTG AAG GAA ATC GAG TTT CTC TCC TGG ACA GAA CCA
TTA GTG TGT AAG ACG AAG GAC TTC CTT TAG CTC AAA GAG AGG ACC TGT CTT GGT
Asn His Thr Phe Cys Phe Leu Lys Glu Ile Glu Phe Leu Ser Trp Thr Glu Pro>
___a___a___a___a___a___a___a___ORF RF[2] ___a___a___a___a___a___a___a___>

      1140      1150      1160      1170      1180
      *      *      *      *      *
TTC GGG ATA GCT TTG GCC ATA TGT GCA GTA CTG GGT GTG CTC TTG ACA GCT TTT
AAG CCC TAT CGA AAC CGG TAT ACA CGT CAT GAC CCA CAC GAG AAC TGT CGA AAA
Phe Gly Ile Ala Leu Ala Ile Cys Ala Val Leu Gly Val Leu Leu Thr Ala Phe>
___a___a___a___a___a___a___a___ORF RF[2] ___a___a___a___a___a___a___a___>

      1190      1200      1210      1220      1230      1240
      *      *      *      *      *      *
GTG ATC GGA GTC TTT GTC AGA TTC CGC AAC ACC CCA ATA GTG AAG GCC ACA AAC
CAC TAG CCT CAG AAA CAG TCT AAG GCG TTG TGG GGT TAT CAC TTC CGG TGT TTG
Val Ile Gly Val Phe Val Arg Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn>
___a___a___a___a___a___a___a___ORF RF[2] ___a___a___a___a___a___a___a___>

      1250      1260      1270      1280      1290
      *      *      *      *      *
CGA GAA CTG TCC TAC GTT CTC CTG TWC TCA CTT ATC TGT TGC TTC TCA AGC TCC
GCT CTT GAC AGG ATG CAA GAG GAC AWG AGT GAA TAG ACA ACG AAG AGT TCG AGG
Arg Glu Leu Ser Tyr Val Leu Leu Xxx Ser Leu Ile Cys Cys Phe Ser Ser Ser>
___a___a___a___a___a___a___a___ORF RF[2] ___a___a___a___a___a___a___a___>

1300
*
CTC AKC TTC ATC GG
GAG TMG AAG TAG CC
Leu Xxx Phe Ile>
___ORF RF[___>

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